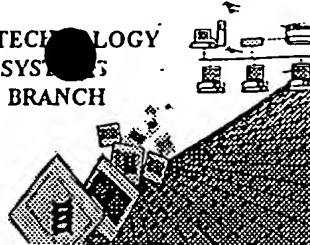n. BRANNER

RAW SEQUENCE LISTING
ERROR REPORT

Re-RUN

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __09/582,719B__
Source: __1600__
Date Processed by STIC: __1/23/03__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/582,719B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 01/23/2003
PATENT APPLICATION: US/09/582,719B TIME: 07:46;49

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01232003\I582719B.raw**

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   5  <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
   9  <120> TITLE OF INVENTION: Novel Sequence Variants of the Human Beta 2-Adrenergic
  10        Receptor Gene and Use Thereof
  14  <130> FILE REFERENCE: 101195-2
  18  <140> CURRENT APPLICATION NUMBER: US 09/582,719B
C--> 20 <141> CURRENT FILING DATE: 2000-08-22
  24  <150> PRIOR APPLICATION NUMBER: PCT/DE98/03818
  26  <151> PRIOR FILING DATE: 1998-12-30
  30  <150> PRIOR APPLICATION NUMBER: DE 197 58 401.2
  32  <151> PRIOR FILING DATE: 1997-12-30
  36  <160> NUMBER OF SEQ ID NOS: 23
  40  <170> SOFTWARE: PatentIn version 3.1
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Wrapped nucleics throughout = See error Summary sheet item 1

ERRORED SEQUENCES

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  44  <210> SEQ ID NO: 1
  46  <211> LENGTH: 3451
  48  <212> TYPE: DNA
  50  <213> ORGANISM: human genomic clone
  54  <220> FEATURE:
  56  <221> NAME/KEY: mutation
  58  <222> LOCATION: (1)..(3451)
  60  <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
  61        mutation
  62        s in positions 159, 245, 565, 934, 1120, ·1221, 1541, 1568,
  63        1633,
W--> 64        1666, 1839, 2078, 2110, 2640, 2826
  68  <400> SEQUENCE: 1
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  70  60
E--> 72 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
  73  120
E--> 75 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
  76  180
E--> 78 tgaaccatat gaatttgcca ttttggtaag tcacagacgc cagatggtgg caatttcaca
  79  240
E--> 81 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
  82  300
E--> 84 ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
  85  360
E--> 87 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
  88  420
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E--> 238 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
     239 3420
E--> 241 gagtgctgtt gcctcccca ctggaaaccg c
     242 3451
     245 <210> SEQ ID NO: 2
     247 <211> LENGTH: 3451
     249 <212> TYPE: DNA
     251 <213> ORGANISM: human genomic clone
     255 <220> FEATURE:
     257 <221> NAME/KEY: mutation
     259 <222> LOCATION: (1)..(3451)
     261 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
     262      mutation
     263      s in positions 1541, 1633, 1666
     267 <400> SEQUENCE: 2
E--> 268 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtacgtg
     269 60
E--> 271 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
     272 120
E--> 274 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
     275 180
E--> 277 tgaaccatat gaatttgcca ttttggtaag tcacagacgc cagatggtgg caatttcaca
     278 240
E--> 280 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
     281 300
E--> 283 ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
     284 360
E--> 286 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
     287 420
E--> 289 cacacaactt tctctctctg tcccaaaata catacttgca taccccgct ccagataaaa
     290 480
E--> 292 tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt
     293 540
E--> 295 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
     296 600
E--> 298 atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
     299 660
E--> 301 gctcgggtga ggcaagttcg gagtacccag atggagacat ccgtgtctgt gtcgctctgg
     302 720
E--> 304 atgcctccaa gccagcgtgt gtttactttc tgtgtgtgtc accatgtctt tgtgcttctg
     305 780
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     308 840
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     311 900
E--> 313 tcagtgtcta tggctgtggt tcggtataag tctgagcatg tctgccaggg tgtatttgtg
     314 960
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     317 1020
```

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

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E--> 395 aattggatag gctatgtcaa ttctggtttc aatcccctta tctactgccg gagcccagat
      396 2580
E--> 398 ttcaggattg ccttccagga gcttctgtgc ctgcgcaggt cttctttgaa ggcctatggg
      399 2640
E--> 401 aatggctact ccagcaacgg caacacaggg gagcagagtg gatatcacgt ggaacaggag
      402 2700
E--> 404 aaagaaaata aactgctgtg tgaagacctc ccaggcacgg aagactttgt gggccatcaa
      405 2760
E--> 407 ggtactgtgc ctagcgataa cattgattca caagggagga attgtagtac aaatgactca
      408 2820
E--> 410 ctgctgtaaa gcagtttttc tactttaaa gacccccccc cccccaacag aacactaaac
      411 2880
E--> 413 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
      414 2940
E--> 416 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
      417 3000
E--> 419 acttatttga gtgattattt gttatttgta cagttcagtt cctctttgca tggaatttgt
      420 3060
E--> 422 aagtttatgt ctaaagagct ttagtcctag aggacctgag tctgctatat tttcatgact
      423 3120
E--> 425 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
      426 3180
E--> 428 gtatctgaag gagattttcc ttcctacacc cttggacttg aggattttga gtatctcgga
      429 3240
E--> 431 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acggggtatt
      432 3300
E--> 434 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
      435 3360
E--> 437 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
      438 3420
E--> 440 gagtgctgtt gcctccccca ctggaaaccg c
      441 3451
      444 <210> SEQ ID NO: 3
      446 <211> LENGTH: 3451
      448 <212> TYPE: DNA
      450 <213> ORGANISM: human genomic clone
      454 <220> FEATURE:
      456 <221> NAME/KEY: mutation
      458 <222> LOCATION: (1)..(3451)
      460 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
      461       mutatio
      462       ns in positions 1541, 1633, 1666
      466 <400> SEQUENCE: 3
E--> 467 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtacgtg
      468 60
E--> 470 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
      471 120
E--> 473 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,719B

DATE: 01/23/2003
TIME: 07:46:49

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
        621 3120
E--> 623 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
        624 3180
E--> 626 gtatctgaag gagattttcc ttcctacacc cttggacttg aggattttga gtatctcgga
        627 3240
E--> 629 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acggggtattt
        630 3300
E--> 632 ttaggcaggg atttgaggag cagcttcagt tgtttttcccg agcaaaggtc taaagtttac
        633 3360
E--> 635 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
        636 3420
E--> 638 gagtgctgtt gcctccccca ctggaaaccg c
        639 3451
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        644 <211> LENGTH: 3451
        646 <212> TYPE: DNA
        648 <213> ORGANISM: human genomic clone
        652 <220> FEATURE:
        654 <221> NAME/KEY: mutation
        656 <222> LOCATION: (1)..(3451)
        658 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
        659       mutation
        660       s in positions 1541, 1633, 1666
        664 <400> SEQUENCE: 4
E--> 665 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtacgtg
        666 60
E--> 668 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
        669 120
E--> 671 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
        672 180
E--> 674 tgaaccatat gaatttgcca ttttggtaag tcacagacgc cagatggtgg caatttcaca
        675 240
E--> 677 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
        678 300
E--> 680 ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
        681 360
E--> 683 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
        684 420
E--> 686 cacacaactt tctctctctg tcccaaaata catacttgca taccccgct ccagataaaa
        687 480
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        690 540
E--> 692 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
        693 600
E--> 695 atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
        696 660
E--> 698 gctcgggtga ggcaagttcg gagtacccag atggagacat ccgtgtctgt gtcgctctgg
        699 720
E--> 701 atgcctccaa gccagcgtgt gtttactttc tgtgtgtgtc accatgtctt tgtgcttctg
```

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01232003\I582719B.raw**

E--> 776 ctggtgatca tggtcttcgt ctactccagg gtctttcagg aggccaaaag gcagctccag
     777 2280

E--> 779 aagattgaca aatctgaggg ccgcttccat gtccagaacc ttagccaggt ggagcaggat
     780 2340

E--> 782 gggcggacgg ggcatggact ccgcagatct tccaagttct gcttgaagga gcacaaagcc
     783 2400

E--> 785 ctcaagacgt taggcatcat catgggcact ttcaccctct gctggctgcc cttcttcatc
     786 2460

E--> 788 gttaacattg tgcatgtgat ccaggataac ctcatccgta aggaagttta catcctccta
     789 2520

E--> 791 aattggatag gctatgtcaa ttctggtttc aatcccctta tctactgccg gagcccagat
     792 2580

E--> 794 ttcaggattg ccttccagga gcttctgtgc ctgcgcaggt cttctttgaa ggcctatggg
     795 2640

E--> 797 aatggctact ccagcaacgg caacacaggg gagcagagtg gatatcacgt ggaacaggag
     798 2700

E--> 800 aaagaaaata aactgctgtg tgaagacctc ccaggcacgg aagactttgt gggccatcaa
     801 2760

E--> 803 ggtactgtgc ctagcgataa cattgattca caagggagga attgtagtac aaatgactca
     804 2820

E--> 806 ctgctgtaaa gcagtttttc tacttttaaa gacccccccc cccccaacag aacactaaac
     807 2880

E--> 809 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
     810 2940

E--> 812 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
     813 3000

E--> 815 acttatttga gtgattattt gttatttgta cagttcagtt cctctttgca tggaatttgt
     816 3060

E--> 818 aagtttatgt ctaaagagct ttagtcctag aggacctgag tctgctatat tttcatgact
     819 3120

E--> 821 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
     822 3180

E--> 824 gtatctgaag gagattttcc ttcctacacc cttggacttg aggattttga gtatctcgga
     825 3240

E--> 827 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acggggtatt
     828 3300

E--> 831 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
     832 3360

E--> 834 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
     835 3420

E--> 837 gagtgctgtt gcctccccca ctggaaaccg c
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     845 <212> TYPE: DNA
     847 <213> ORGANISM: human genomic clone
     851 <220> FEATURE:
     853 <221> NAME/KEY: mutation
     855 <222> LOCATION: (1)..(3451)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,719B

DATE: 01/23/2003
TIME: 07:46:49

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
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        858        mutation
        859        s in positions 1541, 1568, 1633, 1666
        863  <400> SEQUENCE: 5
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     865  60
E--> 867  ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
     868  120
E--> 870  aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
     871  180
E--> 873  tgaaccatat gaatttgcca ttttggtaag tcacagacgc cagatggtgg caatttcaca
     874  240
E--> 876  tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
     877  300
E--> 879  ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
     880  360
E--> 882  gtgagtgatg ccacactctc aagagttaaa aacaaacaa caaaaaatt aaaacaaaag
     883  420
E--> 885  cacacaactt tctctctctg tcccaaaata catacttgca tacccccgct ccagataaaa
     886  480
E--> 888  tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt
     889  540
E--> 891  gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
     892  600
E--> 894  atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
     895  660
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     898  720
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     910  960
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     916  1080
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     922  1200
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     925  1260
E--> 927  gagtgcctcg ccccttcgcg gctgccggcg tgccattggc cgaaagttcc cgtacgtcac
     928  1320
E--> 930  ggcgagggca gttcccctaa agtcctgtgc acataacggg cagaacgcac tgcgaagcgg
```

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01232003\I582719B.raw**

E--> 1005 ctgctgtaaa gcagtttttc tactttttaaa gacccccccc ccccaaоag aacactaaac
     1006 2880
E--> 1008 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
     1009 2940
E--> 1011 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
     1012 3000
E--> 1014 acttatttga gtgattattt gttatttgta cagttcagtt cctctttgca tggaatttgt
     1015 3060
E--> 1017 aagtttatgt ctaaagagct ttagtcctag aggacctgag tctgctatat tttcatgact
     1018 3120
E--> 1020 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
     1021 3180
E--> 1023 gtatctgaag gagattttcc ttcctacacc cttggacttg aggattttga gtatctcgga
     1024 3240
E--> 1026 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acggggtatt
     1027 3300
E--> 1029 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
     1030 3360
E--> 1032 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
     1033 3420
E--> 1035 gagtgctgtt gcctccccca ctggaaaccg c
     1036 3451
     1039 <210> SEQ ID NO: 6
     1041 <211> LENGTH: 3451
     1043 <212> TYPE: DNA
     1045 <213> ORGANISM: human genomic clone
     1049 <220> FEATURE:
     1051 <221> NAME/KEY: mutation
     1053 <222> LOCATION: (1)..(3451)
     1055 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
     1056   mutation
     1057   s in positions 1541, 1568, 1633, 1666
     1061 <400> SEQUENCE: 6
E--> 1062 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtacgtg
     1063 60
E--> 1065 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
     1066 120
E--> 1068 aggatctttt gctttctata gcttcaaaat gttcttaaag ttaagacatt cttaatactc
     1069 180
E--> 1071 tgaaccatat gaatttgcca ttttggtaag tcacagacgc cagatggtgg caatttcaca
     1072 240
E--> 1074 tggcgcaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
     1075 300
E--> 1077 ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
     1078 360
E--> 1080 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
     1081 420
E--> 1083 cacacaactt tctctctctg tcccaaaata catacttgca taccccgct ccagataaaa
     1084 480

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
E--> 1234 gagtgctgtt gcctccccca ctggaaaccg c
     1235 3451
     1238 <210> SEQ ID NO: 7
     1240 <211> LENGTH: 3451
     1242 <212> TYPE: DNA
     1244 <213> ORGANISM: human genomic clone
     1248 <220> FEATURE:
     1250 <221> NAME/KEY: mutation
     1252 <222> LOCATION: (1)..(3451)
     1254 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
     1255        mutation
     1256        s in positions 1541, 1568, 1633, 1666
     1260 <400> SEQUENCE: 7
E--> 1261 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtacgtg
     1262 60
E--> 1264 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
     1265 120
E--> 1267 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
     1268 180
E--> 1270 tgaaccatat gaatttgcca ttttggtaag tcacagacgc cagatggtgg caatttcaca
     1271 240
E--> 1273 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
     1274 300
E--> 1276 ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
     1277 360
E--> 1279 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
     1280 420
E--> 1282 cacacaactt tctctctctg tcccaaaata catacttgca tacccccgct ccagataaaa
     1283 480
E--> 1285 tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt
     1286 540
E--> 1288 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
     1289 600
E--> 1291 atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
     1292 660
E--> 1294 gctcgggtga ggcaagttcg gagtacccag atggagacat ccgtgtctgt gtcgctctgg
     1295 720
E--> 1297 atgcctccaa gccagcgtgt gtttactttc tgtgtgtgtc accatgtctt tgtgcttctg
     1298 780
E--> 1300 ggtgcttctg tgtttgtttc tggccgcgtt tctgtgttgg acaggggtga ctttgtgccg
     1301 840
E--> 1303 gatggcttct gtgtgagagc gcgcgcgagt gtgcatgtcg gtgagctggg agggtgtgtc
     1304 900
E--> 1306 tcagtgtcta tggctgtggt tcggtataag tctgagcatg tctgccaggg tgtatttgtg
     1307 960
E--> 1309 cctgtatgtg cgtgcctcgg tgggcactct cgtttccttc cgaatgtggg gcagtgccgg
     1310 1020
E--> 1312 tgtgctgccc tctgccttga gacctcaagc cgcgcaggcg cccagggcag gcaggtagcg
     1313 1080
```

```
     1388 2580
E--> 1390 ttcaggattg ccttccagga gcttctgtgc ctgcgcaggt cttctttgaa ggcctatggg
     1391 2640
E--> 1393 aatggctact ccagcaacgg caacacaggg gagcagagtg gatatcacgt ggaacaggag
     1394 2700
E--> 1396 aaagaaaata aactgctgtg tgaagacctc ccaggcacgg aagactttgt gggccatcaa
     1397 2760
E--> 1399 ggtactgtgc ctagcgataa cattgattca caagggagga attgtagtac aaatgactca
     1400 2820
E--> 1402 ctgctgtaaa gcagtttttc tacttttaaa gacccccccc cccccaacag aacactaaac
     1403 2880
E--> 1405 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
     1406 2940
E--> 1408 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
     1409 3000
E--> 1411 acttatttga gtgattattt gttatttgta cagttcagtt cctctttgca tggaatttgt
     1412 3060
E--> 1414 aagtttatgt ctaaagagct ttagtcctag aggacctgag tctgctatat tttcatgact
     1415 3120
E--> 1417 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
     1418 3180
E--> 1420 gtatctgaag gagatttttcc ttcctacacc cttggacttg aggattttga gtatctcgga
     1421 3240
E--> 1423 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acggggtatt
     1424 3300
E--> 1426 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
     1427 3360
E--> 1429 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
     1430 3420
E--> 1432 gagtgctgtt gcctccccca ctggaaaccg c
     1433 3451
     1436 <210> SEQ ID NO: 8
     1438 <211> LENGTH: 27
     1440 <212> TYPE: DNA
     1442 <213> ORGANISM: Artificial
     1446 <220> FEATURE:
     1448 <221> NAME/KEY: primer_bind
     1450 <222> LOCATION: (1)..(27)
     1452 <223> OTHER INFORMATION: primer ADRBR-F1 for amplification of fragment I
     1456 <400> SEQUENCE: 8
E--> 1457 tattggccag gatcttttgc tttctat
     1458 27
     1461 <210> SEQ ID NO: 9
     1463 <211> LENGTH: 23
     1465 <212> TYPE: DNA
     1467 <213> ORGANISM: Artificial
     1471 <220> FEATURE:
     1473 <221> NAME/KEY: primer_bind
     1475 <222> LOCATION: (1)..(23)
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,719B

DATE: 01/23/2003
TIME: 07:46:49

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
      1477 <223> OTHER INFORMATION: primer ADRBR-R1 for amplification of fragment I
      1481 <400> SEQUENCE: 9
E-->  1482 taacattaag aacattttga agc
      1483 23
      1486 <210> SEQ ID NO: 10
      1488 <211> LENGTH: 22
      1490 <212> TYPE: DNA
      1492 <213> ORGANISM: Artificial
      1496 <220> FEATURE:
      1498 <221> NAME/KEY: primer_bind
      1500 <222> LOCATION: (1)..(22)
      1502 <223> OTHER INFORMATION: primer ADRBR-F2 for amplification of fragment II
      1506 <400> SEQUENCE: 10
E-->  1507 gcataccccc gctccagata aa
      1508 22
      1511 <210> SEQ ID NO: 11
      1513 <211> LENGTH: 24
      1515 <212> TYPE: DNA
      1517 <213> ORGANISM: Artificial
      1522 <220> FEATURE:
      1524 <221> NAME/KEY: primer_bind
      1526 <222> LOCATION: (1)..(24)
      1528 <223> OTHER INFORMATION: primer ADRBR-R2 for amplification of fragment II
      1532 <400> SEQUENCE: 11
E-->  1533 gcacgcacat acaggcacaa atac
      1534 24
      1537 <210> SEQ ID NO: 12
      1539 <211> LENGTH: 19
      1541 <212> TYPE: DNA
      1543 <213> ORGANISM: Artificial
      1547 <220> FEATURE:
      1549 <221> NAME/KEY: primer_bind
      1551 <222> LOCATION: (1)..(19)
      1553 <223> OTHER INFORMATION: primer ADRBR-F3 for amplification of fragment III
      1557 <400> SEQUENCE: 12
E-->  1558 ggccgcgttt ctgtgttgg
      1559 19
      1562 <210> SEQ ID NO: 13
      1564 <211> LENGTH: 22
      1566 <212> TYPE: DNA
      1568 <213> ORGANISM: Artificial
      1572 <220> FEATURE:
      1574 <221> NAME/KEY: primer_bind
      1576 <222> LOCATION: (1)..(22)
      1578 <223> OTHER INFORMATION: primer ADRBR-R2 for amplification of fragment III
      1582 <400> SEQUENCE: 13
E-->  1583 agtgcgttct gcccgttatg tg
      1584 22
      1587 <210> SEQ ID NO: 14
```

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01232003\I582719B.raw**

```
     1589 <211> LENGTH: 21
     1591 <212> TYPE: DNA
     1593 <213> ORGANISM: Artificial
     1597 <220> FEATURE:
     1599 <221> NAME/KEY: primer_bind
     1601 <222> LOCATION: (1)..(21)
     1603 <223> OTHER INFORMATION: primer ADRBR-F8 for amplification of fragment VIII
     1607 <400> SEQUENCE: 14
E--> 1608 ggtactgtgc ctagcgataa c
     1609 21
     1612 <210> SEQ ID NO: 15
     1614 <211> LENGTH: 28
     1616 <212> TYPE: DNA
     1618 <213> ORGANISM: Artificial
     1622 <220> FEATURE:
     1624 <221> NAME/KEY: primer_bind
     1626 <222> LOCATION: (1)..(28)
     1628 <223> OTHER INFORMATION: primer ADRBR-R8 for amplification of fragment VIII
     1632 <400> SEQUENCE: 15
E--> 1633 taaaataccc cgtgtgagca aataagag
     1634 28
     1637 <210> SEQ ID NO: 16
     1639 <211> LENGTH: 20
     1641 <212> TYPE: DNA
     1643 <213> ORGANISM: Artificial
     1647 <220> FEATURE:
    ·1649 <221> NAME/KEY: primer_bind
     1651 <222> LOCATION: (1)..(20)
     1653 <223> OTHER INFORMATION: primer ADRBR-F4 for amplification of fragment IV
     1657 <400> SEQUENCE: 16
E--> 1658 ggggagggaa aggggaggag
     1659 20
     1662 <210> SEQ ID NO: 17
     1664 <211> LENGTH: 21
     1666 <212> TYPE: DNA
     1668 <213> ORGANISM: Artificial
     1672 <220> FEATURE:
     1674 <221> NAME/KEY: primer_bind
     1676 <222> LOCATION: (1)..(21)
     1678 <223> OTHER INFORMATION: primer ADRBR-R4 for amplification of fragment IV
     1682 <400> SEQUENCE: 17
E--> 1683 ctgccaggcc catgaccaga t
     1684 21
     1687 <210> SEQ ID NO: 18
     1689 <211> LENGTH: 22
     1691 <212> TYPE: DNA
     1693 <213> ORGANISM: Artificial
     1697 <220> FEATURE:
     1699 <221> NAME/KEY: primer_bind
```

```
        1701 <222> LOCATION: (1)..(22)
        1703 <223> OTHER INFORMATION: primer ADRBR-F7 for amplification of fragment VII
        1707 <400> SEQUENCE: 18
E-->    1708 ctggctgccc ttcttcatcg tt
        1709 22
        1712 <210> SEQ ID NO: 19
        1714 <211> LENGTH: 23
        1716 <212> TYPE: DNA
        1718 <213> ORGANISM: Artificial
        1722 <220> FEATURE:
        1724 <221> NAME/KEY: primer_bind
        1726 <222> LOCATION: (1)..(23)
        1728 <223> OTHER INFORMATION: primer ADRBR-R7 for amplification of fragment VII
        1732 <400> SEQUENCE: 19
E-->    1733 taccctaagt taaatagtct gtt
        1734 23
        1737 <210> SEQ ID NO: 20
        1739 <211> LENGTH: 17
        1741 <212> TYPE: DNA
        1743 <213> ORGANISM: Artificial
        1747 <220> FEATURE:
        1749 <221> NAME/KEY: primer_bind
        1751 <222> LOCATION: (1)..(17)
        1753 <223> OTHER INFORMATION: primer ADRBR-F5 for amplification of fragment V
        1757 <400> SEQUENCE: 20
E-->    1758 atgcgccgga ccacgac
        1759 17
```

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:64 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:69 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:268 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
M:254 Repeated in SeqNo=2
L:467 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:665 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4
M:254 Repeated in SeqNo=4
L:864 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
M:254 Repeated in SeqNo=5
L:1062 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:6
M:254 Repeated in SeqNo=6
L:1261 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7
L:1457 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:8
L:1482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:9
L:1507 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:10
L:1533 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:11
L:1558 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:12
L:1583 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:13
L:1608 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:14
L:1633 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:15
L:1658 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:16
L:1683 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:17
L:1708 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:18
L:1733 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:19
L:1758 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:20
L:1783 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:21
L:1809 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:22
L:1835 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:23
M:254 Repeated in SeqNo=23